AMENDMENTS TO THE CLAIMS

1.   (Withdrawn) An isolated polypeptide having the ability to bind to KDR or VEGF/KDR complex comprising an amino acid sequence of one of the following:

Loop Consensus Sequence 15: Cys-X_2-X_3-X_4-X_5-X_6-X_7-Cys (TN8), wherein

X_2 is Ala, Arg, Asn, Asp, Gln, Glu, His, Ile, Lys, Phe, Pro, Ser, Trp or Tyr;

X_3 is Ala, Arg, Asn, Asp, Gln, Glu, Gly, His, Ile, Lys, Met, Phe, Pro, Ser, Thr, Trp, Tyr or Val;

X_4 is Ala, Asn, Asp, Glu, Gly, His, Ile, Leu, Lys, Phe, Pro, Ser, Thr, Trp, Tyr or Val (preferably Asp);

X_5 is Ala, Asp, Glu, Gly, Leu, Phe, Pro, Ser, Thr, Trp or Tyr;

X_6 is Arg, Gln, Glu, Gly, Ile, Leu, Met, Pro, Thr, Trp, Tyr or Val; and

X_7 is Ala, Arg, Gln, Glu, Gly, His, Ile, Leu, Lys, Met, Phe, Trp or Tyr; or

Loop Consensus Sequence 16:Cys-X_2-X_3-X_4-X_5-X_6-X_7-X_8-X_9-X_{10}-X_{11}-Cys (TN12), wherein

X_2 is Arg, Asp, Gln, Glu, Gly, His, Ile, Lys, Met, Thr, Trp, Tyr or Val;

X_3 is Ala, Arg, Asn, Cys, Glu, Ile, Leu, Met, Phe, Ser, Trp or Tyr;

X_4 is Arg, Asn, Asp, Gln, Glu, His, Ile, Leu, Pro, Ser, Thr, Trp, Tyr or Val;

X_5 is Ala, Asn, Asp, Gln, Glu, Gly, His, Met, Phe, Pro, Ser, Trp, Tyr or Val;

X_6 is Asp, Gln, Glu, Gly, His, Ile, Leu, Met, Phe, Pro, Ser, Thr, Trp or Tyr;

X_7 is Ala, Arg, Asn, Asp, Gln, Glu, Gly, Leu, Lys, Met, Phe, Pro, Ser, Thr, Trp, Tyr or Val;

X_8 is Ala, Arg, Asn, Asp, Gln, Glu, Gly, His, Lys, Trp, Tyr or Val;

X_9 is Ala, Arg, Gln, Gly, His, Ile, Lys, Met, Phe, Ser, Thr, Trp, Tyr or Val;

X_{10} is Arg, Gln, Glu, His, Leu, Lys, Met, Phe, Pro, Thr, Trp or Val; and

X_{11} is Arg, Asn, Asp, Glu, His, Ile, Leu, Met, Phe, Pro, Thr, Trp, Tyr or Val; or

Loop Consensus Sequence 17: Cys-X_2-X_3-X_4-Gly-X_6-Cys (TN7), wherein

X_2 is Asn, Asp or Glu;

X_3 is Glu, His, Lys or Phe;

X_4 is Asp, Gln, Leu, Lys, Met or Tyr; and

X_6 is Arg, Gln, Leu, Lys or Val; or

Loop Consensus Sequence 18: Cys-X_2-X_3-X_4-X_5-X_6-X_7-X_8-Cys (TN9), wherein

X_2 is Ala, Asp, Lys, Ser, Trp or Val;

X_3 is Asn, Glu, Gly, His or Leu;

X_4 is Gln, Glu, Gly, Met, Lys, Phe, Tyr or Val;

X_5 is Ala, Asn, Asp, Gly, Leu, Met, Pro, Ser or Thr;

X_6 is His, Pro or Trp;

X_7 is Ala, Gly, His, Leu, Trp or Tyr; and

X_8 is Ala, Asp, Gln, Leu, Met, Thr or Trp; or

Loop Consensus Sequence 19: Cys-X_2-X_3-X_4-X_5-Ser-Gly-Pro-X_9-X_{10}-X_{11}-X_{12}-Cys

(MTN13; SEQ ID NO:1), wherein

X_2 is Asp, Glu, His or Thr;

X_3 is Arg, His, Lys or Phe;

X_4 is Gln, Ile, Lys, Tyr or Val;

X_5 is Gln, Ile, Leu, Met or Phe;

X_9 is Asn, Asp, Gly, His or Tyr;

X_{10} is Gln, Gly, Ser or Thr;

X_{11} is Glu, Lys, Phe or Ser; and

X_{12} is Glu, Ile, Ser or Val.

2.   (Withdrawn) The polypeptide of Claim 1, wherein the polypeptide comprises an amino acid
sequence of one of the following:

Loop Consensus Sequence 20: Cys-X_2-X_3-X_4-X_5-X_6-Tyr-Cys (TN8), wherein

X_2 is Ala, Arg, Glu, Lys or Ser;

X_3 is Ala, Asp, Gln, Glu, Thr or Val;

X_4 is Asp or Glu;

X_5 is Trp or Tyr; and

X_6 is Thr or Tyr; or

Loop Consensus Sequence 21: Cys-X_2-X_3-X_4-Gly-X_6-X_7-Cys (TN8), wherein

X_2 is Asp, Gln or His;

X_3 is His or Tyr;

X_4 is His, Ile or Tyr;

X_6 is Ile, Met or Val; and

X_7 is Gly or Tyr; or

Loop Consensus Sequence 22: Cys-X_2-X_3-X_4-X_5-Gly-X_7-Cys (TN8), wherein

X_2 is Ala, Arg, Asn, Asp, His, Phe, Trp or Tyr;

X_3 is Ala, Asp, Gln, His, Lys, Met, Ser, Thr, Trp, Tyr or Val;

X_4 is Ala, Asn, Asp, Gln, Glu, Gly, His, Ile, Leu, Lys, Pro, Ser, Thr or Val;

X_5 is Asp, Phe, Ser, Thr, Trp or Tyr; and

X_7 is Ala, Arg, Gln, His, Ile, Leu, Lys, Met, Phe, Trp or Tyr.

3.   (Withdrawn) The polypeptide of Claim 1, wherein the polypeptide comprises an amino acid
sequence of one of the following:

Loop Consensus Sequence 23: Cys-X_2-X_3-X_4-X_5-Trp-Gly-Gly-X_9-X_{10}-Cys (SEQ ID NO:3;
TN11), wherein

X_2 is Ala, Phe or Trp;

X_3 is Glu or Lys;

X_4 is Asp, Ser, Trp or Tyr;

X_5 is Phe, Pro or Ser;

X_9 is Gln or Glu; and

X_{10} is Ile, Phe or Val; or

Loop Consensus Sequence 24: Cys-X_2-Glu-X_4-Ser-X_6-Ser-X_8-X_9-X_{10}-Phe-Cys (SEQ ID
NO:15; TN12), wherein

X_2 is His or Tyr;

X_4 is Leu, His or Thr;

X_6 is Asp or Leu;

X_8 is Gly or Val;

X_9 is Thr or Val; and

X_{10} is Arg or Trp; or

Loop Consensus Sequence 25: Cys-X_2-X_3-X_4-X_5-X_6-X_7-Gly-X_9-Trp-X_{11}-Cys (TN12; SEQ ID NO:16), wherein

X_2 is Glu, Met or Thr;

X_3 is Ile, Leu, Met or Phe;

X_4 is Arg, Asp, Glu, Met, Trp or Val;

X_5 is Asn, Gln, Gly, Ser or Val;

X_6 is Glu or Asp;

X_7 is Lys, Ser, Thr or Val;

X_9 is Arg, Gln, Lys or Trp; and

X_{11} is Asn, Leu, Phe or Tyr; or

Loop Consensus Sequence 26: Cys-X_2-X_3-X_4-X_5-X_6-X_7-X_8-X_9-X_{10}-X_{11}-Cys (TN12), wherein

X_2 is Glu or Gly;

X_3 is Trp or Tyr;

X_4 is Ser or Thr;

X_5 is Asn or Gln;

X_6 is Gly or Met;

X_7 is Phe or Tyr;

X_8 is Asp or Gln;

X_9 is Lys or Tyr;

X_{10} is Glu or Thr; and

X_{11} is Glu or Phe.

4.   (Withdrawn) The polypeptide of Claim 1, wherein the polypeptide comprises an amino acid sequence of the following:

Loop Consensus Sequence 27: Cys-X_2-X_3-X_4-Gly-X_6-Cys (TN7), wherein

X_2 is Asn, Asp or Glu;

X_3 is Glu, His, Lys or Phe;

X_4 is Asp, Gln, Leu, Lys, Met or Tyr; and

X_6 is Arg, Gln, Leu, Lys or Val.

5.   (Withdrawn) The polypeptide of Claim 1, wherein the polypeptide comprises an amino acid sequence of the following:

Loop Consensus Sequence 28: Cys-X_2-X_3-X_4-X_5-X_6-X_7-X_8-Cys (TN9), wherein

X_2 is Ala, Lys, Ser, Trp or Val;

X_3 is Asn, Glu, Gly, His or Leu;

X_4 is Glu, Gly, Lys, Met or Tyr;

X_5 is Ala, Asn, Asp, Leu, Met, Pro or Ser;

X_6 is His, Pro or Trp;

X_7 is His, Leu, Trp or Tyr; and

X_8 is Ala, Asp, Gln, Leu, Met, Thr or Trp.

6.   (Withdrawn) The polypeptide of Claim 1, wherein the polypeptide comprises an amino acid sequence of the following:

Loop Consensus Sequence 29: Cys-X_2-X_3-X_4-X_5-Ser-Gly-Pro-X_9-X_{10}-X_{11}-X_{12}-Cys (SEQ ID NO:1; MTN13), wherein

X_2 is Asp, Glu, His or Thr;

X_3 is Arg, His, Lys or Phe;

X_4 is Gln, Ile, Lys, Tyr or Val;

X_5 is Gln, Ile, Leu, Met or Phe;

X_9 is Asn, Asp, Gly, His or Tyr;

X_{10} is Gln, Gly, Ser or Thr;

X_{11} is Glu, Lys, Phe or Ser; and

X_{12} is Glu, Ile, Ser or Val.

7.   (Withdrawn) An isolated polypeptide having the ability to bind to KDR or VEGF/KDR complex comprising an amino acid sequence of one of the following:

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Consensus Sequence 1: X_1-X_2-X_3-Cys-X_5-X_6-X_7-X_8-X_9-X_{10}-Cys-X_{12}-X_{13}-X_{14} (TN8),

wherein

X_1 is Ala, Arg, Asp, Gly, His, Leu, Lys, Pro, Ser, Thr, Trp, Tyr or Val;

X_2 is Asn, Asp, Glu, Gly, Ile, Leu, Lys, Phe, Ser, Thr, Trp, Tyr or Val;

X_3 is Asn, Asp, Gln, Glu, Ile, Leu, Met, Thr, Trp or Val;

X_5 is Ala, Arg, Asn, Asp, Gln, Glu, His, Ile, Lys, Phe, Pro, Ser, Trp or Tyr;

X_6 is Ala, Arg, Asn, Asp, Gln, Glu, Gly, His, Ile, Lys, Met, Phe, Pro, Ser, Thr, Trp, Tyr or Val;

X_7 is Ala, Asn, Asp, Glu, Gly, His, Ile, Leu, Lys, Phe, Pro, Ser, Thr, Trp, Tyr or Val;

X_8 is Ala, Asp, Glu, Gly, Leu, Phe, Pro, Ser, Thr, Trp or Tyr;

X_9 is Arg, Gln, Glu, Gly, Ile, Leu, Met, Pro, Thr, Trp, Tyr or Val;

X_{10} is Ala, Arg, Gln, Glu, Gly, His, Ile, Leu, Lys, Met, Phe, Trp or Tyr;

X_{12} is Arg, Asp, Cys, Gln, Glu, His, Ile, Leu, Lys, Met, Phe, Pro, Ser, Thr, Trp, Tyr or Val;

X_{13} is Arg, Asn, Asp, Gln, Glu, Gly, His, Ile, Leu, Lys, Met, Phe, Ser, Thr, Trp or Tyr; and

X_{14} is Gln, Glu, Gly, His, Ile, Leu, Lys, Met, Phe, Pro, Ser, Thr, Trp or Tyr; or

Consensus Sequence 2: X_1-X_2-X_3-Cys-X_5-X_6-X_7-X_8-X_9-X_{10}-X_{11}-X_{12}-X_{13}-X_{14}-Cys-X_16-X_{17}-X_{18} (TN12), wherein

X_1 is Ala, Asn, Asp, Gly, Leu, Pro, Ser, Trp or Tyr;

X_2 is Ala, Arg, Asn, Asp, Gly, His, Phe, Pro, Ser, Trp or Tyr;

X_3 is Ala, Asn, Asp, Gln, Glu, Gly, His, Leu, Lys, Met, Phe, Ser, Thr, Trp, Tyr or Val;

X_5 is Arg, Asp, Gln, Glu, Gly, His, Ile, Lys, Met, Thr, Trp, Tyr or Val;

X_6 is Ala, Arg, Asn, Cys, Glu, Ile, Leu, Met, Phe, Ser, Trp or Tyr;

X_7 is Arg, Asn, Asp, Gln, Glu, His, Ile, Leu, Pro, Ser, Thr, Trp, Tyr or Val;

X_8 is Ala, Asn, Asp, Gln, Glu, Gly, His, Met, Phe, Pro, Ser, Trp, Tyr or Val;

X_9 is Asp, Gln, Glu, Gly, His, Ile, Leu, Met, Phe, Pro, Ser, Thr, Trp or Tyr;

X_{10} is Ala, Arg, Asn, Asp, Gln, Glu, Gly, Leu, Lys, Met, Phe, Pro, Ser, Thr, Trp, Tyr or Val;

X_{11} is Ala, Arg, Asn, Asp, Gln, Glu, Gly, His, Lys, Trp, Tyr or Val;

X_{12} is Ala, Arg, Gln, Gly, His, Ile, Lys, Met, Phe, Ser, Thr, Trp, Tyr or Val;

X_{13} is Arg, Gln, Glu, His, Leu, Lys, Met, Phe, Pro, Thr, Trp or Val;

X_{14} is Arg, Asn, Asp, Glu, His, Ile, Leu, Met, Phe, Pro, Thr, Trp, Tyr or Val;

X_{16} is Ala, Asn, Asp, Gln, Glu, Gly, Lys, Met, Phe, Ser, Thr, Trp, Tyr or Val;

X_{17} is Arg, Asn, Asp, Cys, Gly, His, Phe, Pro, Ser, Trp or Tyr; and

X_{18} is Ala, Asn, Asp, Gly, His, Leu, Phe, Pro, Ser, Trp or Tyr; or

Consensus Sequence 3: X_1-X_2-X_3-Cys-X_5-X_6-X_7-Gly-X_9-Cys-X_{11}-X_{12}-X_{13} (TN7), wherein

X_1 is Gly or Trp;

X_2 is Ile, Tyr or Val;

X_3 is Gln, Glu, Thr or Trp;

X_5 is Asn, Asp or Glu;

X_6 is Glu, His, Lys or Phe;

X_7 is Asp, Gln, Leu, Lys, Met or Tyr;

X_9 is Arg, Gln, Leu, Lys or Val;

X_{11} is Arg, Phe, Ser, Trp or Val;

X_{12} is Glu, His or Ser; and

X_{13} is Glu, Gly, Trp or Tyr; or

Consensus Sequence 4: X_1-X_2-X_3-Cys-X_5-X_6-X_7-X_8-X_9-X_{10}-X_{11}-Cys-X_{13}-X_{14}-X_{15} (TN9), wherein

X_1 is Arg, Asp, Gly, Ile, Met, Pro or Tyr;

X_2 is Asp, Gly, His, Pro or Trp;

X_3 is Gly, Pro, Phe, Thr or Trp;

X_5 is Ala, Asp, Lys, Ser, Trp or Val;

X_6 is Asn, Glu, Gly, His or Leu;

X_7 is Gln, Glu, Gly, Met, Lys, Phe, Tyr or Val;

X_8 is Ala, Asn, Asp, Gly, Leu, Met, Pro, Ser or Thr;

X_9 is His, Pro or Trp;

X_{10} is Ala, Gly, His, Leu, Trp or Tyr;

X_{11} is Ala, Asp, Gln, Leu, Met, Thr or Trp;

X_{13} is Ala, Lys, Ser, Trp or Tyr;

X_{14} is Asp, Gly, Leu, His, Met, Thr, Trp or Tyr; and

X_{15} is Asn, Gln, Glu, Leu, Met, Pro or Trp; or

Consensus Sequence 5: X_1-X_2-X_3-Cys-X_5-X_6-X_7-X_8-Ser-Gly-Pro-X_{12}-X_{13}-X_{14}-X_{15}-Cys-X_{17}-X_{18}-X_{19} (SEQ ID NO:1; MTN13), wherein

X_1 is Arg, Glu, His, Ser or Trp;

X_2 is Asn, Asp, Leu, Phe, Thr or Val;

X_3 is Arg, Asp, Glu, His, Lys or Thr;

X_5 is Asp, Glu, His or Thr;

X_6 is Arg, His, Lys or Phe;

X_7 is Gln, Ile, Lys, Tyr or Val;

X_8 is Gln, Ile, Leu, Met or Phe;

X_{12} is Asn, Asp, Gly, His or Tyr;

X_{13} is Gln, Gly, Ser or Thr;

X_{14} is Glu, Lys, Phe or Ser;

X_{15} is Glu, Ile, Ser or Val;

X_{17} is Glu, Gly, Lys, Phe, Ser or Val;

X_{18} is Arg, Asn, Ser or Tyr; and

X_{19} is Asp, Gln, Glu, Gly, Met or Tyr.

8.   (Withdrawn) The polypeptide of Claim 7, wherein the polypeptide comprises an amino acid sequence of one of the following:

Consensus Sequence 6: X_1-X_2-X_3-Cys-X_5-X_6-X_7-X_8-X_9-Tyr-Cys-X_{12}-X_{13}-X_{14}, wherein

X_1 is Ala, Arg, Asp, Leu, Lys, Pro, Ser or Val;

X_2 is Asn, Asp, Glu, Lys, Thr or Ser;

X_3 is Ile, Leu, Trp;

X_5 is Ala, Arg, Glu, Lys or Ser;

X_6 is Ala, Asp, Gln, Glu, Thr or Val;

X_7 is Asp or Glu;

X_8 is Trp or Tyr;

X_9 is Thr or Tyr;

X_{12} is Glu, Met, Phe, Trp or Tyr;

X_{13} is Ile, Leu or Met; and

X_{14} is Ile, Leu, Met, Phe or Thr; or

Consensus Sequence 7: Trp-Tyr-Trp-Cys-X_5-X_6-X_7-Gly-X_9-X_{10}-Cys-X_{12}-X_{13}-X_{14} (SEQ ID NO:2), wherein

X_5 is Asp, Gln or His;

X_6 is His or Tyr;

X_7 is Ile, His or Tyr;

X_9 is Ile, Met or Val;

X_{10} is Gly or Tyr;

X_{12} is Asp, Lys or Pro;

X_{13} is Gln, Gly or Trp; and

X_{14} is Phe, Ser or Thr; or

Consensus Sequence 8: X_1-X_2-X_3-Cys-X_5-X_6-X_7-X_8-Gly-X_{10}-Cys-X_{12}-X_{13}-X_{14}, wherein

X_1 is Gly, Leu, His, Thr, Trp, Tyr;

X_2 is Ile, Leu, Thr, Trp or Val;

X_3 is Asp, Glu, Gln, Trp or Thr;

X_5 is Ala, Arg, Asn, Asp, His, Phe, Trp or Tyr;

X_6 is Ala, Asp, Gln, His, Lys, Met, Ser, Thr, Trp, Tyr or Val;

X_7 is Ala, Asn, Asp, Glu, Gly, His, Ile, Leu, Lys, Phe, Pro, Ser, Thr or Val;

X_8 is Asp, Phe, Ser, Thr, Trp or Tyr;

X_{10} is Ala, Arg, Gln, His, Ile, Leu, Lys, Met, Phe, Trp or Tyr;

X_{12} is Arg, Gln, His, Ile, Lys, Met, Phe, Thr, Trp, Tyr or Val;

X_{13} is Arg, Asn, Asp, Glu, His, Met, Pro, Ser or Thr; and

X_{14} is Arg, Gln, Glu, Gly, Phe, Ser, Trp or Tyr.

9.　　　(Withdrawn) The polypeptide of Claim 7, wherein the polypeptide comprises an amino acid sequence of one of the following:

Consensus Sequence 9: X_1-X_2-X_3-Cys-X_5-X_6-X_7-X_8-Trp-Gly-Gly-X_{12}-X_{13}-Cys-X_{15}-X_{16}-X_{17} (SEQ ID NO:3), wherein

X_1 is Ser, Phe, Trp, Tyr or Gly;

X_2 is Arg, Gly, Ser or Trp;

X_3 is Ala, Glu, Ile or Val;

X_5 is Ala, Phe or Trp;

X_6 is Glu or Lys;

X_7 is Asp, Ser or Trp;

X_8 is Phe, Pro or Ser;

X_{12} is Gln or Glu;

X_{13} is Ile, Phe or Val;

X_{15} is Gln, Ile, Leu or Phe;

X_{16} is Arg, Gly or Pro; and

X_{17} is Gln, His, Phe, Ser, Tyr or Val; or

Consensus Sequence 10: Tyr-Pro-X_3-Cys-X_5-Glu-X_7-Ser-X_9-Ser-X_{11}-X_{12}-X_{13}-Phe-Cys-X_{16}-X_{17}-X_{18} (SEQ ID NO:4; TN12), wherein

X_3 is Gly or Trp;

X_5 is His or Tyr;

X_7 is His, Leu or Thr;

X_9 is Asp or Leu;

X_{11} is Gly or Val;

X_{12} is Thr or Val;

X_{13} is Arg or Trp;

X_{16} is Ala or Val;

X_{17} is Asp or Pro; and

X_{18} is Gly or Trp; or

Consensus Sequence 11: X_1-X_2-X_3-Cys-X_5-X_6-X_7-X_8-X_9-X_{10}-Gly-X_{12}-Trp-X_{14}-Cys-X_{16}-X_{17}-X_{18} (SEQ ID NO:5; TN12), wherein

X_1 is Asp, Gly, Pro or Ser;

X_2 is Arg, Asn, Asp, Gly or Ser;

X_3 is Gly, Thr, Trp or Tyr;

X_5 is Glu, Met or Thr;

X_6 is Ile, Leu, Met or Phe;

X_7 is Arg, Asp, Glu, Met, Trp or Val;

X_8 is Asn, Gln, Gly, Ser or Val;

X_9 is Asp or Glu;

X_{10} is Lys, Ser, Thr or Val;

X_{12} is Arg, Gln, Lys or Trp;

X_{14} is Asn, Leu, Phe or Tyr;

X_{16} is Gly, Phe, Ser or Tyr;

X_{17} is Gly, Leu, Pro or Ser; and

X_{18} is Ala, Asp, Pro, Ser, Trp or Tyr; or

Consensus Sequence 12: Asn-Trp-X_3-Cys-X_5-X_6-X_7-X_8-X_9-X_{10}-X_{11}-X_{12}-X_{13}-X_{14}-Cys-X_{16}-X_{17}-X_{18} (SEQ ID NO:6; TN12), wherein

X_3 is Glu or Lys;

X_5 is Glu or Gly;

X_6 is Trp or Tyr;

X_7 is Ser or Thr;

X_8 is Asn or Gln;

X_9 is Gly or Met;

X_{10} is Phe or Tyr;

X_{11} is Asp or Gln;

X_{12} is Lys or Tyr;

X_{13} is Glu or Thr;

X_{14} is Glu or Phe;

X_{16} is Ala or Val;

X_{17} is Arg or Tyr; and

X_{18} is Leu or Pro,

wherein the polypeptide binds KDR or a VEGF/KDR complex.

10. (Currently Amended) An isolated polypeptide having the ability to bind to kinase domain region (KDR) or vascular endothelial growth factor/kinase domain region (VEGF/KDR) complex comprising an amino acid sequence of one of the following:

Consensus Sequence 13: Z_1-X_1-X_2-X_3-X_4-X_5-Z_2; wherein,

Z_1 is a polypeptide of at least one amino acid or is absent;

X_1 is Ala, Asp, Gln or Glu;

X_2 is Ala, Asp, Gln, Glu, Pro;

X_3 is Ala, Leu, Lys, Phe, Pro, Trp or Tyr;

X_4 is Asp, Leu, Ser, Trp, Tyr or Val;

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X_5 is Ala, Arg, Asp, Glu, Gly, Leu, Trp or Tyr; and

Z_2 is a polypeptide of at least one amino acid or is absent; or

Consensus Sequence 14: X_1–X_2–X_3–Tyr–Trp–Glu–X_7–X_8–X_9–Leu (SEQ ID NO:7),

wherein, the sequence can optionally have a N-terminal polypeptide, C-terminal

polypeptide, or a polypeptide at both termini of at least one amino acid; wherein,

X_1 is Asp, Gly or Ser;

X_2 is Ile, Phe or Tyr;

X_3 is Ala, Ser or Val;

X_7 is Gln, Glu, Ile or Val;

X_8 is Ala, Ile or Val and;

X_9 is Ala, Glu, Val or Thr; and, wherein the polypeptide does not contain Cys

residues and wherein the polypeptide is conjugated to one or more detectable labels

or therapeutic agents.

11.　　(Withdrawn) The polypeptide of Claim 7, wherein the polypeptide comprises an amino acid

sequence selected from the group consisting of: SEQ ID NOS: 20-86, 87-136, 187-192, 193-

203, and 207-259.

12.　　(Withdrawn) The polypeptide of Claim 10, wherein the polypeptide comprises an amino

acid sequence selected from the group consisting of: SEQ ID NOS: 137-186.

13.　　(Previously Presented) The polypeptide of claim 10, wherein the polypeptide further

comprises N-terminal and/or C-terminal flanking peptides of one or more amino acids.

14.　　(Previously Presented) The polypeptide of claim 10, wherein the polypeptide comprises a

modification selected from the group consisting of: an amino acid substitution, an amide

bond substitution, a D-amino acid substitution, a glycosylated amino acid, a disulfide bond,

a disulfide mimetic substitution, an amino acid translocation, a retroinverso peptide, a

peptoid, a retro-inverso peptoid, and a synthetic peptide.

15.   (Previously Presented) The polypeptide of claim 10, wherein the polypeptide further comprises a linker or spacer between the polypeptide and the detectable label or the therapeutic agent.

16.   (Original) The polypeptide of Claim 15, wherein the detectable label or the therapeutic agent is selected from the group consisting of: an enzyme, a fluorescent compound, a liposome, an optical dye, one or more paramagnetic metal ions or a superparamagnetic particle, an ultrasound contrast agent and one or more radionuclides.

17.   (Original) The polypeptide of Claim 16, wherein the therapeutic agent or detectable label comprises one or more radionuclides.

18.   (Original) The polypeptide of Claim 17, wherein the radionuclide is selected from the group consisting of: ^{18}F, ^{124}I, ^{125}I, ^{131}I, ^{123}I, ^{77}Br, ^{76}Br, ^{99m}Tc, ^{51}Cr, ^{67}Ga, ^{68}Ga, ^{47}Sc, ^{51}Cr, ^{167}Tm, ^{141}Ce, ^{111}In, ^{168}Yb, ^{175}Yb, ^{140}La, ^{90}Y, ^{88}Y, ^{153}Sm, ^{166}Ho, ^{165}Dy, ^{166}Dy, ^{62}Cu, ^{64}Cu, ^{67}Cu, ^{97}Ru, ^{103}Ru, ^{186}Re, ^{188}Re, ^{203}Pb, ^{211}Bi, ^{212}Bi, ^{213}Bi, ^{214}Bi, ^{105}Rh, ^{109}Pd, ^{117m}Sn, ^{149}Pm, ^{161}Tb, ^{177}Lu, ^{198}Au and ^{199}Au.

19.   (Original) The polypeptide of Claim 18, wherein the therapeutic agent or detectable label further comprises a chelator.

20.   (Original) The polypeptide of Claim 19, wherein the chelator comprises a compound selected from the group consisting of: formula 20, 21, 22, 23a, 23b, 24a, 24b, and 25.

21.   (Original) The polypeptide of Claim 19, wherein the radionuclide is ^{99m}Tc or ^{111}In.

22.   (Original) The polypeptide of Claim 19, wherein the radionuclide is selected from the group consisting of: ^{177}Lu, ^{90}Y, ^{153}Sm and ^{166}Ho.

23.   (Original) The polypeptide of Claim 16, wherein the detectable label comprises an
        ultrasound contrast agent.

24.   (Original) The polypeptide of Claim 23, wherein the ultrasound contrast agent is a
        phospholipid stabilized microbubble or an ultrasound contrast agent comprising a gas.

25.   (Original) The polypeptide of Claim 24, wherein the ultrasound contrast agent comprises a
        fluorinated gas.

26.   (Original) The polypeptide of Claim 16, wherein the detectable label comprises one or more
        paramagnetic metal ions and one or more chelators.

27.   (Withdrawn) The polypeptide of Claim 15, wherein the therapeutic agent is selected from
        the group consisting of: a bioactive agent, a cytotoxic agent, a drug, a chemotherapeutic
        agent and a radiotherapeutic agent.

28-31. (Canceled)

32.   (Withdrawn) A method for isolating phage that bind KDR or a VEGF/KDR complex,
        comprising the steps of:

        (a)   immobilizing a KDR or VEGF/KDR complex target on a solid support;

        (b)   contacting a library of potential KDR or VEGF/KDR complex binding phage
                with the solid support to bind KDR or a VEGF/KDR complex binding phage
                in the library; and

        (c)   removing the unbound portion of the phage library from the solid support,
        thereby isolating phage that bind KDR or a VEGF/KDR complex.

33-52. (Canceled)

1230372.1

53.   (Withdrawn) A recombinant bacteriophage displaying a KDR binding or VEGF/KDR
        complex binding polypeptide, which polypeptide comprises an amino acid sequence of one
        of the following:

Consensus Sequence 1: X_1-X_2-X_3-Cys-X_5-X_6-X_7-X_8-X_9-X_{10}-Cys-X_{12}-X_{13}-X_{14} (TN8),
wherein

      X_1 is Ala, Arg, Asp, Gly, His, Leu, Lys, Pro, Ser, Thr, Trp, Tyr or Val;

      X_2 is Asn, Asp, Glu, Gly, Ile, Leu, Lys, Phe, Ser, Thr, Trp, Tyr or Val;

      X_3 is Asn, Asp, Gln, Glu, Ile, Leu, Met, Thr, Trp or Val;

      X_5 is Ala, Arg, Asn, Asp, Gln, Glu, His, Ile, Lys, Phe, Pro, Ser, Trp or Tyr;

      X_6 is Ala, Arg, Asn, Asp, Gln, Glu, Gly, His, Ile, Lys, Met, Phe, Pro, Ser, Thr, Trp,
Tyr or Val;

      X_7 is Ala, Asn, Asp, Glu, Gly, His, Ile, Leu, Lys, Phe, Pro, Ser, Thr, Trp, Tyr or Val;

      X_8 is Ala, Asp, Glu, Gly, Leu, Phe, Pro, Ser, Thr, Trp or Tyr;

      X_9 is Arg, Gln, Glu, Gly, Ile, Leu, Met, Pro, Thr, Trp, Tyr or Val;

      X_{10} is Ala, Arg, Gln, Glu, Gly, His, Ile, Leu, Lys, Met, Phe, Trp or Tyr;

      X_{12} is Arg, Asp, Cys, Gln, Glu, His, Ile, Leu, Lys, Met, Phe, Pro, Ser, Thr, Trp, Tyr
or Val;

      X_{13} is Arg, Asn, Asp, Gln, Glu, Gly, His, Ile, Leu, Lys, Met, Phe, Ser, Thr, Trp or
Tyr; and

      X_{14} is Gln, Glu, Gly, His, Ile, Leu, Lys, Met, Phe, Pro, Ser, Thr, Trp or Tyr; or

Consensus Sequence 2: X_1-X_2-X_3-Cys-X_5-X_6-X_7-X_8-X_9-X_{10}-X_{11}-X_{12}-X_{13}-X_{14}-Cys-X_{16}-X_{17}-
X_{18} (TN12), wherein

      X_1 is Ala, Asn, Asp, Gly, Leu, Pro, Ser, Trp or Tyr;

      X_2 is Ala, Arg, Asn, Asp, Gly, His, Phe, Pro, Ser, Trp or Tyr;

      X_3 is Ala, Asn, Asp, Gln, Glu, Gly, His, Leu, Lys, Met, Phe, Ser, Thr, Trp, Tyr or
Val;

      X_5 is Arg, Asp, Gln, Glu, Gly, His, Ile, Lys, Met, Thr, Trp, Tyr or Val;

      X_6 is Ala, Arg, Asn, Cys, Glu, Ile, Leu, Met, Phe, Ser, Trp or Tyr;

X_7 is Arg, Asn, Asp, Gln, Glu, His, Ile, Leu, Pro, Ser, Thr, Trp, Tyr or Val;

X_8 is Ala, Asn, Asp, Gln, Glu, Gly, His, Met, Phe, Pro, Ser, Trp, Tyr or Val;

X_9 is Asp, Gln, Glu, Gly, His, Ile, Leu, Met, Phe, Pro, Ser, Thr, Trp or Tyr;

X_{10} is Ala, Arg, Asn, Asp, Gln, Glu, Gly, Leu, Lys, Met, Phe, Pro, Ser, Thr, Trp, Tyr or Val;

X_{11} is Ala, Arg, Asn, Asp, Gln, Glu, Gly, His, Lys, Trp, Tyr or Val;

X_{12} is Ala, Arg, Gln, Gly, His, Ile, Lys, Met, Phe, Ser, Thr, Trp, Tyr or Val;

X_{13} is Arg, Gln, Glu, His, Leu, Lys, Met, Phe, Pro, Thr, Trp or Val;

X_{14} is Arg, Asn, Asp, Glu, His, Ile, Leu, Met, Phe, Pro, Thr, Trp, Tyr or Val;

X_{16} is Ala, Asn, Asp, Gln, Glu, Gly, Lys, Met, Phe, Ser, Thr, Trp, Tyr or Val;

X_{17} is Arg, Asn, Asp, Cys, Gly, His, Phe, Pro, Ser, Trp or Tyr; and

X_{18} is Ala, Asn, Asp, Gly, His, Leu, Phe, Pro, Ser, Trp or Tyr; or

Consensus Sequence 3: X_1-X_2-X_3-Cys-X_5-X_6-X_7-Gly-X_9-Cys-X_{11}-X_{12}-X_{13} (TN7), wherein

X_1 is Gly or Trp;

X_2 is Ile, Tyr or Val;

X_3 is Gln, Glu, Thr or Trp;

X_5 is Asn, Asp or Glu;

X_6 is Glu, His, Lys or Phe;

X_7 is Asp, Gln, Leu, Lys, Met or Tyr;

X_9 is Arg, Gln, Leu, Lys or Val;

X_{11} is Arg, Phe, Ser, Trp or Val;

X_{12} is Glu, His or Ser; and

X_{13} is Glu, Gly, Trp or Tyr; or

Consensus Sequence 4: X_1-X_2-X_3-Cys-X_5-X_6-X_7-X_8-X_9-X_{10}-X_{11}-Cys-X_{13}-X_{14}-X_{15} (TN9), wherein

X_1 is Arg, Asp, Gly, Ile, Met, Pro or Tyr;

X_2 is Asp, Gly, His, Pro or Trp;

X_3 is Gly, Pro, Phe, Thr or Trp;

X_5 is Ala, Asp, Lys, Ser, Trp or Val;

X_6 is Asn, Glu, Gly, His or Leu;

X_7 is Gln, Glu, Gly, Met, Lys, Phe, Tyr or Val;

X_8 is Ala, Asn, Asp, Gly, Leu, Met, Pro, Ser or Thr;

X_9 is His, Pro or Trp;

X_{10} is Ala, Gly, His, Leu, Trp or Tyr;

X_{11} is Ala, Asp, Gln, Leu, Met, Thr or Trp;

X_{13} is Ala, Lys, Ser, Trp or Tyr;

X_{14} is Asp, Gly, Leu, His, Met, Thr, Trp or Tyr; and

X_{15} is Asn, Gln, Glu, Leu, Met, Pro or Trp; or

Consensus Sequence 5: X_1-X_2-X_3-Cys-X_5-X_6-X_7-X_8-Ser-Gly-Pro-X_{12}-X_{13}-X_{14}-X_{15}-Cys-X_{17}-X_{18}-X_{19} (SEQ ID NO:1; MTN13), wherein

X_1 is Arg, Glu, His, Ser or Trp;

X_2 is Asn, Asp, Leu, Phe, Thr or Val;

X_3 is Arg, Asp, Glu, His, Lys or Thr;

X_5 is Asp, Glu, His or Thr;

X_6 is Arg, His, Lys or Phe;

X_7 is Gln, Ile, Lys, Tyr or Val;

X_8 is Gln, Ile, Leu, Met or Phe;

X_{12} is Asn, Asp, Gly, His or Tyr;

X_{13} is Gln, Gly, Ser or Thr;

X_{14} is Glu, Lys, Phe or Ser;

X_{15} is Glu, Ile, Ser or Val;

X_{17} is Glu, Gly, Lys, Phe, Ser or Val;

X_{18} is Arg, Asn, Ser or Tyr; and

X_{19} is Asp, Gln, Glu, Gly, Met or Tyr,

and wherein the polypeptide is displayed on the surface of the recombinant bacteriophage.

54.   (Withdrawn) A magnetic resonance imaging contrast agent comprising a KDR or

VEGF/KDR complex binding polypeptide comprising an amino acid sequence of one of the

following:

Consensus Sequence 1: X_1-X_2-X_3-Cys-X_5-X_6-X_7-X_8-X_9-X_{10}-Cys-X_{12}-X_{13}-X_{14} (TN8),

wherein

X_1 is Ala, Arg, Asp, Gly, His, Leu, Lys, Pro, Ser, Thr, Trp, Tyr or Val;

X_2 is Asn, Asp, Glu, Gly, Ile, Leu, Lys, Phe, Ser, Thr, Trp, Tyr or Val;

X_3 is Asn, Asp, Gln, Glu, Ile, Leu, Met, Thr, Trp or Val;

X_5 is Ala, Arg, Asn, Asp, Gln, Glu, His, Ile, Lys, Phe, Pro, Ser, Trp or Tyr;

X_6 is Ala, Arg, Asn, Asp, Gln, Glu, Gly, His, Ile, Lys, Met, Phe, Pro, Ser, Thr, Trp,

Tyr or Val;

X_7 is Ala, Asn, Asp, Glu, Gly, His, Ile, Leu, Lys, Phe, Pro, Ser, Thr, Trp, Tyr or Val;

X_8 is Ala, Asp, Glu, Gly, Leu, Phe, Pro, Ser, Thr, Trp or Tyr;

X_9 is Arg, Gln, Glu, Gly, Ile, Leu, Met, Pro, Thr, Trp, Tyr or Val;

X_{10} is Ala, Arg, Gln, Glu, Gly, His, Ile, Leu, Lys, Met, Phe, Trp or Tyr;

X_{12} is Arg, Asp, Cys, Gln, Glu, His, Ile, Leu, Lys, Met, Phe, Pro, Ser, Thr, Trp, Tyr

or Val;

X_{13} is Arg, Asn, Asp, Gln, Glu, Gly, His, Ile, Leu, Lys, Met, Phe, Ser, Thr, Trp or

Tyr; and

X_{14} is Gln, Glu, Gly, His, Ile, Leu, Lys, Met, Phe, Pro, Ser, Thr, Trp or Tyr; or

Consensus Sequence 2: X_1-X_2-X_3-Cys-X_5-X_6-X_7-X_8-X_9-X_{10}-X_{11}-X_{12}-X_{13}-X_{14}-Cys-X_{16}-X_{17}-

X_{18} (TN12), wherein

X_1 is Ala, Asn, Asp, Gly, Leu, Pro, Ser, Trp or Tyr;

X_2 is Ala, Arg, Asn, Asp, Gly, His, Phe, Pro, Ser, Trp or Tyr;

X_3 is Ala, Asn, Asp, Gln, Glu, Gly, His, Leu, Lys, Met, Phe, Ser, Thr, Trp, Tyr or

Val;

X_5 is Arg, Asp, Gln, Glu, Gly, His, Ile, Lys, Met, Thr, Trp, Tyr or Val;

X_6 is Ala, Arg, Asn, Cys, Glu, Ile, Leu, Met, Phe, Ser, Trp or Tyr;

X_7 is Arg, Asn, Asp, Gln, Glu, His, Ile, Leu, Pro, Ser, Thr, Trp, Tyr or Val;

X_8 is Ala, Asn, Asp, Gln, Glu, Gly, His, Met, Phe, Pro, Ser, Trp, Tyr or Val;

X_9 is Asp, Gln, Glu, Gly, His, Ile, Leu, Met, Phe, Pro, Ser, Thr, Trp or Tyr;

X_{10} is Ala, Arg, Asn, Asp, Gln, Glu, Gly, Leu, Lys, Met, Phe, Pro, Ser, Thr, Trp, Tyr or Val;

X_{11} is Ala, Arg, Asn, Asp, Gln, Glu, Gly, His, Lys, Trp, Tyr or Val;

X_{12} is Ala, Arg, Gln, Gly, His, Ile, Lys, Met, Phe, Ser, Thr, Trp, Tyr or Val;

X_{13} is Arg, Gln, Glu, His, Leu, Lys, Met, Phe, Pro, Thr, Trp or Val;

X_{14} is Arg, Asn, Asp, Glu, His, Ile, Leu, Met, Phe, Pro, Thr, Trp, Tyr or Val;

X_{16} is Ala, Asn, Asp, Gln, Glu, Gly, Lys, Met, Phe, Ser, Thr, Trp, Tyr or Val;

X_{17} is Arg, Asn, Asp, Cys, Gly, His, Phe, Pro, Ser, Trp or Tyr; and

X_{18} is Ala, Asn, Asp, Gly, His, Leu, Phe, Pro, Ser, Trp or Tyr; or

Consensus Sequence 3: X_1-X_2-X_3-Cys-X_5-X_6-X_7-Gly-X_9-Cys-X_{11}-X_{12}-X_{13} (TN7), wherein

X_1 is Gly or Trp;

X_2 is Ile, Tyr or Val;

X_3 is Gln, Glu, Thr or Trp;

X_5 is Asn, Asp or Glu;

X_6 is Glu, His, Lys or Phe;

X_7 is Asp, Gln, Leu, Lys, Met or Tyr;

X_9 is Arg, Gln, Leu, Lys or Val;

X_{11} is Arg, Phe, Ser, Trp or Val;

X_{12} is Glu, His or Ser; and

X_{13} is Glu, Gly, Trp or Tyr; or

Consensus Sequence 4: X_1-X_2-X_3-Cys-X_5-X_6-X_7-X_8-X_9-X_{10}-X_{11}-Cys-X_{13}-X_{14}-X_{15} (TN9), wherein

X_1 is Arg, Asp, Gly, Ile, Met, Pro or Tyr;

X_2 is Asp, Gly, His, Pro or Trp;

X_3 is Gly, Pro, Phe, Thr or Trp;

X_5 is Ala, Asp, Lys, Ser, Trp or Val;

X_6 is Asn, Glu, Gly, His or Leu;

X_7 is Gln, Glu, Gly, Met, Lys, Phe, Tyr or Val;

X_8 is Ala, Asn, Asp, Gly, Leu, Met, Pro, Ser or Thr;

X_9 is His, Pro or Trp;

X_{10} is Ala, Gly, His, Leu, Trp or Tyr;

X_{11} is Ala, Asp, Gln, Leu, Met, Thr or Trp;

X_{13} is Ala, Lys, Ser, Trp or Tyr;

X_{14} is Asp, Gly, Leu, His, Met, Thr, Trp or Tyr; and

X_{15} is Asn, Gln, Glu, Leu, Met, Pro or Trp; or

Consensus Sequence 5: X_1-X_2-X_3-Cys-X_5-X_6-X_7-X_8-Ser-Gly-Pro-X_{12}-X_{13}-X_{14}-X_{15}-Cys-X_{17}-X_{18}-X_{19} (SEQ ID NO:1; MTN13), wherein

X_1 is Arg, Glu, His, Ser or Trp;

X_2 is Asn, Asp, Leu, Phe, Thr or Val;

X_3 is Arg, Asp, Glu, His, Lys or Thr;

X_5 is Asp, Glu, His or Thr;

X_6 is Arg, His, Lys or Phe;

X_7 is Gln, Ile, Lys, Tyr or Val;

X_8 is Gln, Ile, Leu, Met or Phe;

X_{12} is Asn, Asp, Gly, His or Tyr;

X_{13} is Gln, Gly, Ser or Thr;

X_{14} is Glu, Lys, Phe or Ser;

X_{15} is Glu, Ile, Ser or Val;

X_{17} is Glu, Gly, Lys, Phe, Ser or Val;

X_{18} is Arg, Asn, Ser or Tyr; and

X_{19} is Asp, Gln, Glu, Gly, Met or Tyr,

wherein the polypeptide is coupled to at least one chelator capable of complexing a paramagnetic metal or at least one superparamagnetic particle, and wherein the polypeptide optionally comprises an N-terminal and/or C-terminal flanking peptide.

55-75. (Canceled)

1230372.1

76.   (Withdrawn) A multimeric polypeptide construct having the ability to bind to KDR or

VEGF/KDR complex comprising at least one amino acid selected from the group consisting

of:

Loop Consensus Sequence 15: Cys-X_2-X_3-X_4-X_5-X_6-X_7-Cys (TN8), wherein

   X2 is Ala, Arg, Asn, Asp, Gln, Glu, His, Ile, Lys, Phe, Pro, Ser, Trp or Tyr;

   X3 is Ala, Arg, Asn, Asp, Gln, Glu, Gly, His, Ile, Lys, Met, Phe, Pro, Ser, Thr, Trp,

   Tyr or Val;

   X4 is Ala, Asn, Asp, Glu, Gly, His, Ile, Leu, Lys, Phe, Pro, Ser, Thr, Trp, Tyr or Val;

   X5 is Ala, Asp, Glu, Gly, Leu, Phe, Pro, Ser, Thr, Trp or Tyr;

   X6 is Arg, Gln, Glu, Gly, Ile, Leu, Met, Pro, Thr, Trp, Tyr or Val; and

   X7 is Ala, Arg, Gln, Glu, Gly, His, Ile, Leu, Lys, Met, Phe, Trp or Tyr; or

Loop Consensus Sequence 16: Cys-X_2-X_3-X_4-X_5-X_6-X_7-X_8-X_9-X_{10}-X_{11}-Cys (TN12), wherein

   X2 is Arg, Asp, Gln, Glu, Gly, His, Ile, Lys, Met, Thr, Trp, Tyr or Val;

   X3 is Ala, Arg, Asn, Cys, Glu, Ile, Leu, Met, Phe, Ser, Trp or Tyr;

   X4 is Arg, Asn, Asp, Gln, Glu, His, Ile, Leu, Pro, Ser, Thr, Trp, Tyr or Val;

   X5 is Ala, Asn, Asp, Gln, Glu, Gly, His, Met, Phe, Pro, Ser, Trp, Tyr or Val;

   X6 is Asp, Gln, Glu, Gly, His, Ile, Leu, Met, Phe, Pro, Ser, Thr, Trp or Tyr;

   X7 is Ala, Arg, Asn, Asp, Gln, Glu, Gly, Leu, Lys, Met, Phe, Pro, Ser, Thr, Trp, Tyr

   or Val;

   X8 is Ala, Arg, Asn, Asp, Gln, Glu, Gly, His, Lys, Trp, Tyr or Val;

   X9 is Ala, Arg, Gln, Gly, His, Ile, Lys, Met, Phe, Ser, Thr, Trp, Tyr or Val;

   X10 is Arg, Gln, Glu, His, Leu, Lys, Met, Phe, Pro, Thr, Trp or Val; and

   X11 is Arg, Asn, Asp, Glu, His, Ile, Leu, Met, Phe, Pro, Thr, Trp, Tyr or Val; or

Loop Consensus Sequence 17: Cys-X_2-X_3-X_4-Gly-X_6-Cys (TN7), wherein

   X2 is Asn, Asp or Glu;

   X3 is Glu, His, Lys or Phe;

   X4 is Asp, Gln, Leu, Lys, Met or Tyr; and

X6 is Arg, Gln, Leu, Lys or Val; or

Consensus Sequence IV: Cys-X_2-X_3-X_4-X_5-X_6-X_7-X_8-Cys (TN9), wherein

X2 is Ala, Asp, Lys, Ser, Trp or Val;

X3 is Asn, Glu, Gly, His or Leu;

X4 is Gln, Glu, Gly, Met, Lys, Phe, Tyr or Val;

X5 is Ala, Asn, Asp, Gly, Leu, Met, Pro, Ser or Thr;

X6 is His, Pro or Trp;

X7 is Ala, Gly, His, Leu, Trp or Tyr; and

X8 is Ala, Asp, Gln, Leu, Met, Thr or Trp; or

Loop Consensus Sequence 18: Cys-X_2-X_3-X_4-X_5-X_6-X_7-X_8-Cys (TN9), wherein

X_2 is Ala, Asp, Lys, Ser, Trp or Val;

X_3 is Asn, Glu, Gly, His or Leu;

X_4 is Gln, Glu, Gly, Met, Lys, Phe, Tyr or Val;

X_5 is Ala, Asn, Asp, Gly, Leu, Met, Pro, Ser or Thr;

X_6 is His, Pro or Trp;

X_7 is Ala, Gly, His, Leu, Trp or Tyr; and

X_8 is Ala, Asp, Gln, Leu, Met, Thr or Trp; or

Loop Consensus Sequence 19: Cys-X_2-X_3-X_4-X_5-Ser-Gly-Pro-X_9-X_{10}-X_{11}-X_{12}-Cys

(MTN13; SEQ ID NO:1), wherein

X_2 is Asp, Glu, His or Thr;

X_3 is Arg, His, Lys or Phe;

X_4 is Gln, Ile, Lys, Tyr or Val;

X_5 is Gln, Ile, Leu, Met or Phe;

X_9 is Asn, Asp, Gly, His or Tyr;

X_{10} is Gln, Gly, Ser or Thr;

X_{11} is Glu, Lys, Phe or Ser; and

X_{12} is Glu, Ile, Ser or Val.

77.   (Canceled)

1230372.1

78.   (Currently Amended) A multimeric polypeptide construct having the ability to bind to KDR or VEGF/KDR complex comprising at least one amino acid sequence of one of the following:

Consensus Sequence 13: Z_1-X_1-X_2-X_3-X_4-X_5-Z_2; wherein,

Z_1 is a polypeptide of at least one amino acid or is absent;

X_1 is Ala, Asp, Gln or Glu;

X_2 is Ala, Asp, Gln, Glu, Pro;

X_3 is Ala, Leu, Lys, Phe, Pro, Trp or Tyr;

X_4 is Asp, Leu, Ser, Trp, Tyr or Val;

X_5 is Ala, Arg, Asp, Glu, Gly, Leu, Trp or Tyr; and

Z_2 is a polypeptide of at least one amino acid or is absent; or

Consensus Sequence 14: X_1-X_2-X_3-Tyr-Trp-Glu-X_7-X_8-X_9-Leu (SEQ ID NO:7), wherein, the sequence can optionally have a N-terminal polypeptide, C-terminal polypeptide, or a polypeptide at both termini of at least one amino acid; wherein,

X_1 is Asp, Gly or Ser;

X_2 is Ile, Phe or Tyr;

X_3 is Ala, Ser or Val;

X_7 is Gln, Glu, Ile or Val;

X_8 is Ala, Ile or Val _and_;

X_9 is Ala, Glu, Val or Thr, wherein the polypeptide does not contain Cys residues.

79-157.   (Canceled)

158.   (Withdrawn) A method of detecting KDR or VEGF/KDR complex in an animal or human subject and optionally imaging at least a portion of the animal or human subject comprising the steps of:

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(a)   detectably labeling a multimeric polypeptide construct of one of Claims 76,

or 78;

(b)   administering to the subject the labeled multimeric polypeptide construct;

and,

(c)   detecting the labeled multimeric polypeptide construct in the subject,

and, optionally, constructing an image..

159-174.   (Canceled)

175.   (Withdrawn) A multimeric polypeptide having the ability to bind to KDR or VEGF/KDR

complex selected from the group consisting of: D30 and D31.

176-194.   (Canceled)

195.   (Withdrawn) A method of inhibiting VEGF activation of KDR comprising administering to

an animal or human subject in need of treatment for such condition a polypeptide having the ability

to bind to KDR or VEGF/KDR complex, or a multimeric polypeptide construct comprising at least

one ploypeptide having the ability to bind to KDR or VEGF/KDR complex, said polypeptide

comprising an amino acid sequence of one of the following:

Consensus Sequence 1: X_1-X_2-X_3-Cys-X_5-X_6-X_7-X_8-X_9-X_{10}-Cys-X_{12}-X_{13}-X_{14} (TN8),

wherein

X_1 is Ala, Arg, Asp, Gly, His, Leu, Lys, Pro, Ser, Thr, Trp, Tyr or Val;

X_2 is Asn, Asp, Glu, Gly, Ile, Leu, Lys, Phe, Ser, Thr, Trp, Tyr or Val;

X_3 is Asn, Asp, Gln, Glu, Ile, Leu, Met, Thr, Trp or Val;

X_5 is Ala, Arg, Asn, Asp, Gln, Glu, His, Ile, Lys, Phe, Pro, Ser, Trp or Tyr;

X_6 is Ala, Arg, Asn, Asp, Gln, Glu, Gly, His, Ile, Lys, Met, Phe, Pro, Ser, Thr, Trp,

Tyr or Val;

X_7 is Ala, Asn, Asp, Glu, Gly, His, Ile, Leu, Lys, Phe, Pro, Ser, Thr, Trp, Tyr or Val;

X_8 is Ala, Asp, Glu, Gly, Leu, Phe, Pro, Ser, Thr, Trp or Tyr;

X_9 is Arg, Gln, Glu, Gly, Ile, Leu, Met, Pro, Thr, Trp, Tyr or Val;

X_{10} is Ala, Arg, Gln, Glu, Gly, His, Ile, Leu, Lys, Met, Phe, Trp or Tyr;

X_{12} is Arg, Asp, Cys, Gln, Glu, His, Ile, Leu, Lys, Met, Phe, Pro, Ser, Thr, Trp, Tyr or Val;

X_{13} is Arg, Asn, Asp, Gln, Glu, Gly, His, Ile, Leu, Lys, Met, Phe, Ser, Thr, Trp or Tyr; and

X_{14} is Gln, Glu, Gly, His, Ile, Leu, Lys, Met, Phe, Pro, Ser, Thr, Trp or Tyr; or

Consensus Sequence 2: X_1-X_2-X_3-Cys-X_5-X_6-X_7-X_8-X_9-X_{10}-X_{11}-X_{12}-X_{13}-X_{14}-Cys-X_{16}-X_{17}-X_{18} (TN12), wherein

X_1 is Ala, Asn, Asp, Gly, Leu, Pro, Ser, Trp or Tyr;

X_2 is Ala, Arg, Asn, Asp, Gly, His, Phe, Pro, Ser, Trp or Tyr;

X_3 is Ala, Asn, Asp, Gln, Glu, Gly, His, Leu, Lys, Met, Phe, Ser, Thr, Trp, Tyr or Val;

X_5 is Arg, Asp, Gln, Glu, Gly, His, Ile, Lys, Met, Thr, Trp, Tyr or Val;

X_6 is Ala, Arg, Asn, Cys, Glu, Ile, Leu, Met, Phe, Ser, Trp or Tyr;

X_7 is Arg, Asn, Asp, Gln, Glu, His, Ile, Leu, Pro, Ser, Thr, Trp, Tyr or Val;

X_8 is Ala, Asn, Asp, Gln, Glu, Gly, His, Met, Phe, Pro, Ser, Trp, Tyr or Val;

X_9 is Asp, Gln, Glu, Gly, His, Ile, Leu, Met, Phe, Pro, Ser, Thr, Trp or Tyr;

X_{10} is Ala, Arg, Asn, Asp, Gln, Glu, Gly, Leu, Lys, Met, Phe, Pro, Ser, Thr, Trp, Tyr or Val;

X_{11} is Ala, Arg, Asn, Asp, Gln, Glu, Gly, His, Lys, Trp, Tyr or Val;

X_{12} is Ala, Arg, Gln, Gly, His, Ile, Lys, Met, Phe, Ser, Thr, Trp, Tyr or Val;

X_{13} is Arg, Gln, Glu, His, Leu, Lys, Met, Phe, Pro, Thr, Trp or Val;

X_{14} is Arg, Asn, Asp, Glu, His, Ile, Leu, Met, Phe, Pro, Thr, Trp, Tyr or Val;

X_{16} is Ala, Asn, Asp, Gln, Glu, Gly, Lys, Met, Phe, Ser, Thr, Trp, Tyr or Val;

X_{17} is Arg, Asn, Asp, Cys, Gly, His, Phe, Pro, Ser, Trp or Tyr; and

X_{18} is Ala, Asn, Asp, Gly, His, Leu, Phe, Pro, Ser, Trp or Tyr; or

Consensus Sequence 3: X_1-X_2-X_3-Cys-X_5-X_6-X_7-Gly-X_9-Cys-X_{11}-X_{12}-X_{13} (TN7), wherein

X_1 is Gly or Trp;

X_2 is Ile, Tyr or Val;

X_3 is Gln, Glu, Thr or Trp;

X_5 is Asn, Asp or Glu;

X_6 is Glu, His, Lys or Phe;

X_7 is Asp, Gln, Leu, Lys, Met or Tyr;

X_9 is Arg, Gln, Leu, Lys or Val;

X_{11} is Arg, Phe, Ser, Trp or Val;

X_{12} is Glu, His or Ser; and

X_{13} is Glu, Gly, Trp or Tyr; or

Consensus Sequence 4: X_1-X_2-X_3-Cys-X_5-X_6-X_7-X_8-X_9-X_{10}-X_{11}-Cys-X_{13}-X_{14}-X_{15} (TN9), wherein

X_1 is Arg, Asp, Gly, Ile, Met, Pro or Tyr;

X_2 is Asp, Gly, His, Pro or Trp;

X_3 is Gly, Pro, Phe, Thr or Trp;

X_5 is Ala, Asp, Lys, Ser, Trp or Val;

X_6 is Asn, Glu, Gly, His or Leu;

X_7 is Gln, Glu, Gly, Met, Lys, Phe, Tyr or Val;

X_8 is Ala, Asn, Asp, Gly, Leu, Met, Pro, Ser or Thr;

X_9 is His, Pro or Trp;

X_{10} is Ala, Gly, His, Leu, Trp or Tyr;

X_{11} is Ala, Asp, Gln, Leu, Met, Thr or Trp;

X_{13} is Ala, Lys, Ser, Trp or Tyr;

X_{14} is Asp, Gly, Leu, His, Met, Thr, Trp or Tyr; and

X_{15} is Asn, Gln, Glu, Leu, Met, Pro or Trp;

Consensus Sequence 5: X_1-X_2-X_3-Cys-X_5-X_6-X_7-X_8-Ser-Gly-Pro-X_{12}-X_{13}-X_{14}-X_{15}-Cys-X_{17}-X_{18}-X_{19} (SEQ ID NO:1; MTN13), wherein

X_1 is Arg, Glu, His, Ser or Trp;

X_2 is Asn, Asp, Leu, Phe, Thr or Val;

X_3 is Arg, Asp, Glu, His, Lys or Thr;

X_5 is Asp, Glu, His or Thr;

X_6 is Arg, His, Lys or Phe;

X_7 is Gln, Ile, Lys, Tyr or Val;

X_8 is Gln, Ile, Leu, Met or Phe;

X_{12} is Asn, Asp, Gly, His or Tyr;

X_{13} is Gln, Gly, Ser or Thr;

X_{14} is Glu, Lys, Phe or Ser;

X_{15} is Glu, Ile, Ser or Val;

X_{17} is Glu, Gly, Lys, Phe, Ser or Val;

X_{18} is Arg, Asn, Ser or Tyr; and

X_{19} is Asp, Gln, Glu, Gly, Met or Tyr;

Consensus Sequence 13: Z_1-X_1-X_2-X_3-X_4-X_5-Z_2 (Lin20); wherein,

Z_1 is a polypeptide of at least one amino acid or is absent;

X_1 is Ala, Asp, Gln or Glu;

X_2 is Ala, Asp, Gln, Glu, Pro;

X_3 is Ala, Leu, Lys, Phe, Pro, Trp or Tyr;

X_4 is Asp, Leu, Ser, Trp, Tyr or Val;

X_5 is Ala, Arg, Asp, Glu, Gly, Leu, Trp or Tyr; and

Z_2 is a polypeptide of at least one amino acid or is absent;

Consensus Sequence 14: X_1–X_2–X_3–Tyr–Trp–Glu–X_7–X_8–X_9–Leu (Lin20; SEQ ID NO:7),

wherein, the sequence can optionally have a N-terminal polypeptide, C-terminal

polypeptide, or a polypeptide at both termini of at least one amino acid; wherein,

X_1 is Asp, Gly or Ser;

X_2 is Ile, Phe or Tyr;

X_3 is Ala, Ser or Val;

X_7 is Gln, Glu, Ile or Val;

X_8 is Ala, Ile or Val;

X_9 is Ala, Glu, Val or Thr;

Loop Consensus Sequence 15: Cys-X_2-X_3-X_4-X_5-X_6-X_7-Cys (TN8), wherein

X_2 is Ala, Arg, Asn, Asp, Gln, Glu, His, Ile, Lys, Phe, Pro, Ser, Trp or Tyr;

X_3 is Ala, Arg, Asn, Asp, Gln, Glu, Gly, His, Ile, Lys, Met, Phe, Pro, Ser, Thr, Trp, Tyr or Val;

X_4 is Ala, Asn, Asp, Glu, Gly, His, Ile, Leu, Lys, Phe, Pro, Ser, Thr, Trp, Tyr or Val (preferably Asp);

X_5 is Ala, Asp, Glu, Gly, Leu, Phe, Pro, Ser, Thr, Trp or Tyr;

X_6 is Arg, Gln, Glu, Gly, Ile, Leu, Met, Pro, Thr, Trp, Tyr or Val; and

X_7 is Ala, Arg, Gln, Glu, Gly, His, Ile, Leu, Lys, Met, Phe, Trp or Tyr; or

Loop Consensus Sequence 16: Cys-X_2-X_3-X_4-X_5-X_6-X_7-X_8-X_9-X_{10}-X_{11}-Cys (TN12), wherein

X_2 is Arg, Asp, Gln, Glu, Gly, His, Ile, Lys, Met, Thr, Trp, Tyr or Val;

X_3 is Ala, Arg, Asn, Cys, Glu, Ile, Leu, Met, Phe, Ser, Trp or Tyr;

X_4 is Arg, Asn, Asp, Gln, Glu, His, Ile, Leu, Pro, Ser, Thr, Trp, Tyr or Val;

X_5 is Ala, Asn, Asp, Gln, Glu, Gly, His, Met, Phe, Pro, Ser, Trp, Tyr or Val;

X_6 is Asp, Gln, Glu, Gly, His, Ile, Leu, Met, Phe, Pro, Ser, Thr, Trp or Tyr;

X_7 is Ala, Arg, Asn, Asp, Gln, Glu, Gly, Leu, Lys, Met, Phe, Pro, Ser, Thr, Trp, Tyr or Val;

X_8 is Ala, Arg, Asn, Asp, Gln, Glu, Gly, His, Lys, Trp, Tyr or Val;

X_9 is Ala, Arg, Gln, Gly, His, Ile, Lys, Met, Phe, Ser, Thr, Trp, Tyr or Val;

X_{10} is Arg, Gln, Glu, His, Leu, Lys, Met, Phe, Pro, Thr, Trp or Val; and

X_{11} is Arg, Asn, Asp, Glu, His, Ile, Leu, Met, Phe, Pro, Thr, Trp, Tyr or Val; or

Loop Consensus Sequence 17: Cys-X_2-X_3-X_4-Gly-X_6-Cys (TN7), wherein

X_2 is Asn, Asp or Glu;

X_3 is Glu, His, Lys or Phe;

X_4 is Asp, Gln, Leu, Lys, Met or Tyr; and

X_6 is Arg, Gln, Leu, Lys or Val; or

Loop Consensus Sequence 18: Cys-X_2-X_3-X_4-X_5-X_6-X_7-X_8-Cys (TN9), wherein

X_2 is Ala, Asp, Lys, Ser, Trp or Val;

X_3 is Asn, Glu, Gly, His or Leu;

X_4 is Gln, Glu, Gly, Met, Lys, Phe, Tyr or Val;

X_5 is Ala, Asn, Asp, Gly, Leu, Met, Pro, Ser or Thr;

X_6 is His, Pro or Trp;

X_7 is Ala, Gly, His, Leu, Trp or Tyr; and

X_8 is Ala, Asp, Gln, Leu, Met, Thr or Trp; or

Loop Consensus Sequence 19: Cys-X_2-X_3-X_4-X_5-Ser-Gly-Pro-X_9-X_{10}-X_{11}-X_{12}-Cys

(MTN13; SEQ ID NO:1), wherein

X_2 is Asp, Glu, His or Thr;

X_3 is Arg, His, Lys or Phe;

X_4 is Gln, Ile, Lys, Tyr or Val;

X_5 is Gln, Ile, Leu, Met or Phe;

X_9 is Asn, Asp, Gly, His or Tyr;

X_{10} is Gln, Gly, Ser or Thr;

X_{11} is Glu, Lys, Phe or Ser; and

X_{12} is Glu, Ile, Ser or Val.

196-197.   (Canceled)

198.   (Currently Amended) An isolated polypeptide having the ability to bind to kinase domain region (KDR) or vascular endothelial growth factor/kinase domain region (VEGF/KDR) complex comprising an amino acid sequence of SEQ ID NO.:304, SEQ ID NO.:305, SEQ ID NO.:306, SEQ ID NO.:307, SEQ ID NO.:308, SEQ ID NO.:309, or SEQ ID NO.:310 SEQ ID NO:304, SEQ ID NO:305, SEQ ID NO:306, SEQ ID NO:307, SEQ ID NO:308, SEQ ID NO:309, or SEQ ID NO:310.

199.   (Currently Amended) The isolated polypeptide of claim 198, wherein the polypeptide consists of the amino acid sequence SEQ ID NO.:310 SEQ ID NO:310.